

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/540,845
Source: PCF
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PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/540,845

DATE: 03/01/2006

TIME: 14:00:43

Input Set : E:\ARS-113 - sequence listing.txt
 Output Set: N:\CRF4\03012006\J540845.raw

3 <110> APPLICANT: Applied Research Systems ARS Holding N.V.
 5 <120> TITLE OF INVENTION: NOVEL PREADIPOCYTE FACTOR-1-LIKE POLYPEPTIDES
 7 <130> FILE REFERENCE: PCT/812
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/540,845
 C--> 9 <141> CURRENT FILING DATE: 2005-06-27
 9 <150> PRIOR APPLICATION NUMBER: US60/436,815
 10 <151> PRIOR FILING DATE: 2002-12-27
 12 <160> NUMBER OF SEQ ID NOS: 18
 14 <170> SOFTWARE: PatentIn version 3.2
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 1663
 18 <212> TYPE: DNA
 19 <213> ORGANISM: homo sapiens
 22 <220> FEATURE:
 23 <221> NAME/KEY: CDS
 24 <222> LOCATION: (122)..(1180)
 26 <400> SEQUENCE: 1
 27 agacggcaac gtggacagga agaagcggag ggcgaggagg agcagaggag cacacagatg 60
 29 aagcagggtgt ccacgcgtcc ggccgtccat ccgtccgtcc ctccctggggc cggcgctgac 120
 31 c atg ccc agc ggc tgc cgc tgc ctg cat ctc gtg tgc ctg ttg tgc att 169
 32 Met Pro Ser Gly Cys Arg Cys Leu His Leu Val Cys Leu Leu Cys Ile
 33 1 5 10 15
 35 ctg ggg gct ccc ggt cag cct gtc cga gcc gat gac tgc agc tcc cac 217
 36 Leu Gly Ala Pro Gly Gln Pro Val Arg Ala Asp Asp Cys Ser Ser His
 37 20 25 30
 39 tgt gac ctg gcc cac ggc tgc tgt gca cct gac ggc tcc tgc agg tgt 265
 40 Cys Asp Leu Ala His Gly Cys Cys Ala Pro Asp Gly Ser Cys Arg Cys
 41 35 40 45
 43 gac ccg ggc tgg gag ggg ctg cac tgt gag cgc tgt gtg agg atg cct 313
 44 Asp Pro Gly Trp Glu Gly Leu His Cys Glu Arg Cys Val Arg Met Pro
 45 50 55 60
 47 ggc tgc cag cac ggt acc tgc cac cag cca tgg cag tgc atc tgc cac 361
 48 Gly Cys Gln His Gly Thr Cys His Gln Pro Trp Gln Cys Ile Cys His
 49 65 70 75 80
 51 agt ggc tgg gca ggc aag ttc tgt gac aaa ggc ttc cat ggg cgt gac 409
 52 Ser Gly Trp Ala Gly Lys Phe Cys Asp Lys Gly Phe His Gly Arg Asp
 53 85 90 95
 55 tgc gag cgc aag gct gga ccc tgt gaa cag gca ggc tcc cca tgc cgc 457
 56 Cys Glu Arg Lys Ala Gly Pro Cys Glu Gln Ala Gly Ser Pro Cys Arg
 57 100 105 110
 59 aat ggc ggg cag tgc cag gac gac cag ggc ttt gct ctc aac ttc acg 505
 60 Asn Gly Gly Gln Cys Gln Asp Asp Gln Gly Phe Ala Leu Asn Phe Thr
 61 115 120 125

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63	tgc	cgc	tgc	ttg	gtg	ggc	ttt	gtg	ggt	gcc	cgc	tgt	gag	gta	aat	gtg	553
64	Cys	Arg	Cys	Leu	Val	Gly	Phe	Val	Gly	Ala	Arg	Cys	Glu	Val	Asn	Val	
65	130			135				140									
67	gat	gac	tgc	ctg	atg	cg	cct	tgt	gct	aac	ggt	gcc	acc	tgc	ctt	gac	601
68	Asp	Asp	Cys	Leu	Met	Arg	Pro	Cys	Ala	Asn	Gly	Ala	Thr	Cys	Leu	Asp	
69	145			150			155			160							
71	ggc	ata	aac	cgc	ttc	tcc	tgc	ctc	tgt	cct	gag	ggc	ttt	gct	gga	cgc	649
72	Gly	Ile	Asn	Arg	Phe	Ser	Cys	Leu	Cys	Pro	Glu	Gly	Phe	Ala	Gly	Arg	
73		165			170			175									
75	ttc	tgc	acc	atc	aac	ctg	gat	gac	tgt	gcc	agc	cgc	cca	tgc	cag	aga	697
76	Phe	Cys	Thr	Ile	Asn	Leu	Asp	Asp	Cys	Ala	Ser	Arg	Pro	Cys	Gln	Arg	
77		180			185			190									
79	ggg	gcc	cgc	tgt	cg	gac	cgt	gtc	cac	gac	ttc	gac	tc	tc	tc	ccc	745
80	Gly	Ala	Arg	Cys	Arg	Asp	Arg	Val	His	Asp	Phe	Asp	Cys	Leu	Cys	Pro	
81		195			200			205									
83	agt	ggc	tat	ggt	ggc	aag	acc	tgt	gag	ctt	gtc	tta	cct	gtc	cca	gac	793
84	Ser	Gly	Tyr	Gly	Gly	Lys	Thr	Cys	Glu	Leu	Val	Leu	Pro	Val	Pro	Asp	
85		210			215			220									
87	ccc	cca	acc	aca	gtg	gac	acc	cct	cta	ggg	ccc	acc	tca	gct	gta	gtg	841
88	Pro	Pro	Thr	Thr	Val	Asp	Thr	Pro	Leu	Gly	Pro	Thr	Ser	Ala	Val	Val	
89	225		230			235			240								
91	gta	cct	gcc	acg	ggg	cca	gcc	ccc	cac	agc	gca	ggg	gct	ggt	ctg	ctg	889
92	Val	Pro	Ala	Thr	Gly	Pro	Ala	Pro	His	Ser	Ala	Gly	Ala	Gly	Leu	Leu	
93		245			250			255									
95	cgg	atc	tca	gtg	aag	gag	gtg	gtg	cg	agg	caa	gag	gct	ggg	cta	ggt	937
96	Arg	Ile	Ser	Val	Lys	Glu	Val	Val	Arg	Arg	Gln	Glu	Ala	Gly	Leu	Gly	
97		260			265			270									
99	gag	cct	agc	ttg	gtg	gcc	ctg	gtg	ttt	ggg	gcc	ctc	act	gct	gcc	985	
100	Glu	Pro	Ser	Leu	Val	Ala	Leu	Val	Val	Phe	Gly	Ala	Leu	Thr	Ala	Ala	
101		275			280			285									
103	ctg	gtt	ctg	gct	act	gtg	ttg	ctg	acc	ctg	agg	gcc	tgg	cgc	cgg	ggt	1033
104	Leu	Val	Leu	Ala	Thr	Val	Leu	Leu	Thr	Leu	Arg	Ala	Trp	Arg	Arg	Gly	
105		290			295			300									
107	gtc	tgc	ccc	cct	gga	ccc	tgt	tgc	tac	cct	gcc	cca	cac	tat	gct	cca	1081
108	Val	Cys	Pro	Pro	Gly	Pro	Cys	Cys	Tyr	Pro	Ala	Pro	His	Tyr	Ala	Pro	
109	305		310			315			320								
111	gcg	tgc	cag	gac	cag	gag	tgt	cag	gtc	agc	atg	ctg	cca	gca	ggg	ctc	1129
112	Ala	Cys	Gln	Asp	Gln	Glu	Cys	Gln	Val	Ser	Met	Leu	Pro	Ala	Gly	Leu	
113		325			330			335									
115	ccc	ctg	cca	cgt	gac	ttg	ccc	cct	gag	cct	gga	aag	acc	aca	gca	ctg	1177
116	Pro	Leu	Pro	Arg	Asp	Leu	Pro	Pro	Glu	Pro	Gly	Lys	Thr	Thr	Ala	Leu	
117		340			345			350									
119	tga	tggaggtggg	ggctttctgg	cccccttcct	caccccttc	acccttc	caga	ccat	1230								
121	ctggagtggt	ccgttctcac	cacccttcag	cttgggtaca	cacacagagg	agacccatc	ccat	1290									
123	ctcacacca	aaatattatt	tttttaatac	acagaatgt	agatggatt	ttatcaaata											1350
125	aaactatgaa	aatgcaggatg	ggcttcctatg	ccagaaaaac	ccacccgtcg	ttccatcgatgc											1410
127	aagaggggcca	gagcagaggc	ctgggtctgg	ggaagcctca	ggatgctgcc	caccaaggag											1470
129	tgatttccaa	agagtaatcc	agggtgcct	tttcccttct	ggggaaatgt	ggagaggtag											1530
131	agccccagag	gagaatgtaa	acaaggcagcc	agcacctctg	tataggcccc	gcctggatca											1590

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133 gagagagggg agaactctgc agggtgtggg attgggctca gggacctccg agtgaggcag 1650
135 ggactccctg ctg 1663
138 <210> SEQ ID NO: 2
139 <211> LENGTH: 352
140 <212> TYPE: PRT
141 <213> ORGANISM: homo sapiens
143 <400> SEQUENCE: 2
145 Met Pro Ser Gly Cys Arg Cys Leu His Leu Val Cys Leu Leu Cys Ile
146 1 5 10 15
149 Leu Gly Ala Pro Gly Gln Pro Val Arg Ala Asp Asp Cys Ser Ser His
150 20 25 30
153 Cys Asp Leu Ala His Gly Cys Cys Ala Pro Asp Gly Ser Cys Arg Cys
154 35 40 45
157 Asp Pro Gly Trp Glu Gly Leu His Cys Glu Arg Cys Val Arg Met Pro
158 50 55 60
161 Gly Cys Gln His Gly Thr Cys His Gln Pro Trp Gln Cys Ile Cys His
162 65 70 75 80
165 Ser Gly Trp Ala Gly Lys Phe Cys Asp Lys Gly Phe His Gly Arg Asp
166 85 90 95
169 Cys Glu Arg Lys Ala Gly Pro Cys Glu Gln Ala Gly Ser Pro Cys Arg
170 100 105 110
173 Asn Gly Gly Gln Cys Gln Asp Asp Gln Gly Phe Ala Leu Asn Phe Thr
174 115 120 125
177 Cys Arg Cys Leu Val Gly Phe Val Gly Ala Arg Cys Glu Val Asn Val
178 130 135 140
181 Asp Asp Cys Leu Met Arg Pro Cys Ala Asn Gly Ala Thr Cys Leu Asp
182 145 150 155 160
185 Gly Ile Asn Arg Phe Ser Cys Leu Cys Pro Glu Gly Phe Ala Gly Arg
186 165 170 175
189 Phe Cys Thr Ile Asn Leu Asp Asp Cys Ala Ser Arg Pro Cys Gln Arg
190 180 185 190
193 Gly Ala Arg Cys Arg Asp Arg Val His Asp Phe Asp Cys Leu Cys Pro
194 195 200 205
197 Ser Gly Tyr Gly Lys Thr Cys Glu Leu Val Leu Pro Val Pro Asp
198 210 215 220
201 Pro Pro Thr Thr Val Asp Thr Pro Leu Gly Pro Thr Ser Ala Val Val
202 225 230 235 240
205 Val Pro Ala Thr Gly Pro Ala Pro His Ser Ala Gly Ala Gly Leu Leu
206 245 250 255
209 Arg Ile Ser Val Lys Glu Val Val Arg Arg Gln Glu Ala Gly Leu Gly
210 260 265 270
213 Glu Pro Ser Leu Val Ala Leu Val Val Phe Gly Ala Leu Thr Ala Ala
214 275 280 285
217 Leu Val Leu Ala Thr Val Leu Leu Thr Leu Arg Ala Trp Arg Arg Gly
218 290 295 300
221 Val Cys Pro Pro Gly Pro Cys Cys Tyr Pro Ala Pro His Tyr Ala Pro
222 305 310 315 320
225 Ala Cys Gln Asp Gln Glu Cys Gln Val Ser Met Leu Pro Ala Gly Leu
226 325 330 335

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229 Pro Leu Pro Arg Asp Leu Pro Pro Glu Pro Gly Lys Thr Thr Ala Leu
230 340 345 350
233 <210> SEQ ID NO: 3
234 <211> LENGTH: 332
235 <212> TYPE: PRT
236 <213> ORGANISM: homo sapiens
238 <400> SEQUENCE: 3
240 Gly Gln Pro Val Arg Ala Asp Asp Cys Ser Ser His Cys Asp Leu Ala
241 1 5 10 15
244 His Gly Cys Cys Ala Pro Asp Gly Ser Cys Arg Cys Asp Pro Gly Trp
245 20 25 30
248 Glu Gly Leu His Cys Glu Arg Cys Val Arg Met Pro Gly Cys Gln His
249 35 40 45
252 Gly Thr Cys His Gln Pro Trp Gln Cys Ile Cys His Ser Gly Trp Ala
253 50 55 60
256 Gly Lys Phe Cys Asp Lys Gly Phe His Gly Arg Asp Cys Glu Arg Lys
257 65 70 75 80
260 Ala Gly Pro Cys Glu Gln Ala Gly Ser Pro Cys Arg Asn Gly Gln
261 85 90 95
264 Cys Gln Asp Asp Gln Gly Phe Ala Leu Asn Phe Thr Cys Arg Cys Leu
265 100 105 110
268 Val Gly Phe Val Gly Ala Arg Cys Glu Val Asn Val Asp Asp Cys Leu
269 115 120 125
272 Met Arg Pro Cys Ala Asn Gly Ala Thr Cys Leu Asp Gly Ile Asn Arg
273 130 135 140
276 Phe Ser Cys Leu Cys Pro Glu Gly Phe Ala Gly Arg Phe Cys Thr Ile
277 145 150 155 160
280 Asn Leu Asp Asp Cys Ala Ser Arg Pro Cys Gln Arg Gly Ala Arg Cys
281 165 170 175
284 Arg Asp Arg Val His Asp Phe Asp Cys Leu Cys Pro Ser Gly Tyr Gly
285 180 185 190
288 Gly Lys Thr Cys Glu Leu Val Leu Pro Val Pro Asp Pro Pro Thr Thr
289 195 200 205
292 Val Asp Thr Pro Leu Gly Pro Thr Ser Ala Val Val Val Pro Ala Thr
293 210 215 220
296 Gly Pro Ala Pro His Ser Ala Gly Ala Gly Leu Leu Arg Ile Ser Val
297 225 230 235 240
300 Lys Glu Val Val Arg Arg Gln Glu Ala Gly Leu Gly Glu Pro Ser Leu
301 245 250 255
304 Val Ala Leu Val Val Phe Gly Ala Leu Thr Ala Ala Leu Val Leu Ala
305 260 265 270
308 Thr Val Leu Leu Thr Leu Arg Ala Trp Arg Arg Gly Val Cys Pro Pro
309 275 280 285
312 Gly Pro Cys Cys Tyr Pro Ala Pro His Tyr Ala Pro Ala Cys Gln Asp
313 290 295 300
316 Gln Glu Cys Gln Val Ser Met Leu Pro Ala Gly Leu Pro Leu Pro Arg
317 305 310 315 320
320 Asp Leu Pro Pro Glu Pro Gly Lys Thr Thr Ala Leu
321 325 330

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Input Set : E:\ARS-113 - sequence listing.txt
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324 <210> SEQ ID NO: 4
325 <211> LENGTH: 358
326 <212> TYPE: PRT
327 <213> ORGANISM: homo sapiens
329 <400> SEQUENCE: 4
331 Met Pro Ser Gly Cys Arg Cys Leu His Leu Val Cys Leu Leu Cys Ile
332 1 5 10 15
335 Leu Gly Ala Pro Gly Gln Pro Val Arg Ala Asp Asp Cys Ser Ser His
336 20 25 30
339 Cys Asp Leu Ala His Gly Cys Cys Ala Pro Asp Gly Ser Cys Arg Cys
340 35 40 45
343 Asp Pro Gly Trp Glu Gly Leu His Cys Glu Arg Cys Val Arg Met Pro
344 50 55 60
347 Gly Cys Gln His Gly Thr Cys His Gln Pro Trp Gln Cys Ile Cys His
348 65 70 75 80
351 Ser Gly Trp Ala Gly Lys Phe Cys Asp Lys Gly Phe His Gly Arg Asp
352 85 90 95
355 Cys Glu Arg Lys Ala Gly Pro Cys Glu Gln Ala Gly Ser Pro Cys Arg
356 100 105 110
359 Asn Gly Gly Gln Cys Gln Asp Asp Gln Gly Phe Ala Leu Asn Phe Thr
360 115 120 125
363 Cys Arg Cys Leu Val Gly Phe Val Gly Ala Arg Cys Glu Val Asn Val
364 130 135 140
367 Asp Asp Cys Leu Met Arg Pro Cys Ala Asn Gly Ala Thr Cys Leu Asp
368 145 150 155 160
371 Gly Ile Asn Arg Phe Ser Cys Leu Cys Pro Glu Gly Phe Ala Gly Arg
372 165 170 175
375 Phe Cys Thr Ile Asn Leu Asp Asp Cys Ala Ser Arg Pro Cys Gln Arg
376 180 185 190
379 Gly Ala Arg Cys Arg Asp Arg Val His Asp Phe Asp Cys Leu Cys Pro
380 195 200 205
383 Ser Gly Tyr Gly Lys Thr Cys Glu Leu Val Leu Pro Val Pro Asp
384 210 215 220
387 Pro Pro Thr Thr Val Asp Thr Pro Leu Gly Pro Thr Ser Ala Val Val
388 225 230 235 240
391 Val Pro Ala Thr Gly Pro Ala Pro His Ser Ala Gly Ala Gly Leu Leu
392 245 250 255
395 Arg Ile Ser Val Lys Glu Val Val Arg Arg Gln Glu Ala Gly Leu Gly
396 260 265 270
399 Glu Pro Ser Leu Val Ala Leu Val Val Phe Gly Ala Leu Thr Ala Ala
400 275 280 285
403 Leu Val Leu Ala Thr Val Leu Leu Thr Leu Arg Ala Trp Arg Arg Gly
404 290 295 300
407 Val Cys Pro Pro Gly Pro Cys Cys Tyr Pro Ala Pro His Tyr Ala Pro
408 305 310 315 320
411 Ala Cys Gln Asp Gln Glu Cys Gln Val Ser Met Leu Pro Ala Gly Leu
412 325 330 335
415 Pro Leu Pro Arg Asp Leu Pro Pro Glu Pro Gly Lys Thr Thr Ala Leu
416 340 345 350

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/540,845

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Input Set : E:\ARS-113 - sequence listing.txt
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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date